

- Ahmad, D. see Sylvestre, M., 439  
Akhmanova, A.S. see Spiridonova, V.A., 153  
Akiba, T. see Hamana, K., 450  
Alaboudi, A. see Lämmler, C., 614  
Alexander, M. see Sinclair, J.L., 578  
Aleya, L. see Marvalín, O., 706  
Allmansberger, R., Bokranz, M., Kröckel, L., Schallenberg, J., and Klein, A. Conserved gene structures and expression signals in methanogenic archaeobacteria, 52  
Amat, A.S., and Torrella, F. Isolation and characterization of marine and salt pond halophilic bdellovibrios, 771  
Amils, R., Ramírez, L., Sanz, J.L., Marín, I., Pisabarro, A.G., and Ureña, D. The use of functional analysis of the ribosome as a tool to determine archaeobacterial phylogeny, 141  
Anderson, J.B. see Horgen, P.A., 492  
Anderson, T.R., and Montie, T.C. Flagellar antibody stimulated opsonophagocytosis of *Pseudomonas aeruginosa* associated with response to either *a*- or *b*-type flagellar antigen, 890  
Arimitsu, Y., Moribayashi, A., and Goto, N. Skin reaction to lipids from avirulent strain Shibaura of *Lepto-spira interrogans* serovar *copenhageni*, 1009  
Armon, R. see Payment, P., 932  
Arndt, E. see Kimura, M., 195  
Arnold, P.M. see Powell, I.B., 860  
Arnold, R.R. see Bortner, C.A., 1048  
Asselin, A. see Leclerc, D., 749  
Atlas, R.M. see Mormile, M.R., 603  
Atlas, R.M. see Steffan, R.J., 681  
Auer, J., Lechner, K., and Böck, A. Gene organization and structure of two transcriptional units from *Methanococcus* coding for ribosomal proteins and elongation factors, 200  
Barbotin, J.-N. see Saucedo, J.E.N., 1118  
Barran, L.R. see Chan, Y.-K., 737  
Bashan, Y., Levanony, H., and Mitiku, G. Changes in proton efflux of intact wheat roots induced by *Azospirillum brasilense* Cd, 691  
Bashan, Y., and Levanony, H. Factors affecting adsorption of *Azospirillum brasilense* Cd to root hairs as compared with root surface of wheat, 936  
Baumeister, W., Wildhaber, I., and Phipps, B.M. Principles of organization in eubacterial and archaeobacterial surface proteins, 215  
Beauchamp, E.G. see Paul, J.W., 754  
Beckler, G.S. see Thomm, M., 30  
Bédard, J., and Lefebvre, G.M. L-Alanine and inosine enhancement of glucose triggering in *Bacillus megaterium* spores, 760  
Benhamou, N. Ultrastructural study of galacturonic acid distribution in some pathogenic fungi using gold-complexed *Aplysia depilans* gonad lectin, 349  
Benhamou, N. see Chalifour, F.-P., 821  
Bentjen, S.A. see Fredrickson, J.K., 867  
Benton, W.H. see Hurst, C.J., 474  
Bertrand, J.C. see Bonin, P., 1061  
Bérubé, A. see Payment, P., 932  
Betlach, M.C., Shand, R.F., and Leong, D.M. Regulation of the bacterio-opsin gene of a halophilic archaeobacterium, 134  
Beveridge, T.J. see Ferris, F.G., 744  
Beveridge, T.J. see Mayers, I.T., 764  
Bezanson, G.S. see Dalton, M.T., 819  
Bigby, D., and Kropinski, A.M.B. Isolation and characterization of a *Pseudomonas aeruginosa* bacteriophage with a very limited host range, 630  
Bishop, P.E. see Premakumar, R., 344  
Blaseio, U. see Pfeifer, F., 96  
Bleakley, B.H., and Crawford, D.L. The effects of varying moisture and nutrient levels on the transfer of a conjugative plasmid between *Streptomyces* species in soil, 544  
Böck, A. see Auer, J., 200  
Bokranz, M. see Allmansberger, R., 52  
Bolton, H., Jr. see Fredrickson, J.K., 867  
Bonin, P., Gilewicz, M., and Bertrand, J.C. Effects of oxygen on each step of denitrification on *Pseudomonas nautica*, 1061  
Boonkitticharoen, V., Ehrhardt, J.C., and Kirchner, P.T. Bacterial growth kinetics: modelling and evaluation of two-compartment radioassay, 874  
Bortner, C.A., Arnold, R.R., and Miller, R.D. Bactericidal effect of lactoferrin on *Legionella pneumophila*: effect of the physiological state of the organism, 1048  
Bos, C.J. see Debets, A.J.M., 982  
Bosch, A. see Girones, R., 1015  
Brandon, L.D. see Thompson, L.D., 36  
Breen, A. see Steffan, R.J., 681  
Breil, B. see Widden, P., 469  
Breitmayer, V.A. see Gauthier, M.J., 379  
Bromfield, E.S.P. see Chan, Y.-K., 737  
Brooks, J.B. see Pine, L., 245  
Brooks, J.B. see Daneshvar, M.I., 786  
Brown, J.W. see Thomm, M., 30  
Bruhn, J.N. see Richter, D.L., 1055  
Brunel, A., and Gouet, P. Intestinal microflora of the newborn rat as related to mammary, faecal, and vaginal *Staphylococci* strains isolated from the dam, 989  
Bryant, R.D., and Laishley, E.J. Evidence for proton motive force dependent transport of selenite by *Clostridium pasteurianum*, 481  
Butler, M.J., Lazarovits, G., Higgins, V.J., and Lachance, M.-A. Identification of a black yeast isolated from oak bark as belonging to the genus *Phaeococcomyces* sp. Analysis of melanin produced by the yeast, 728  
Caldwell, D.R. Effects of methanol on the growth of gastrointestinal anaerobes, 313  
Calleja, G.B. see Johnson, B.F., 1081  
Cammarano, P., Tiboni, O., and Sanangelantoni, A.M. Phylogenetic conservation of antigenic determinants in archaeobacterial elongation factors (Tu proteins), 2  
Campubí, S., Regué, M., and Tomás, J. The influence of lipopolysaccharide on the transformation efficiency of *Klebsiella pneumoniae*, 735

- Cao, K. see Ree, H.K., 124
- Carson, D.B., and Cooney, J.J. Characterization of partially purified microbodies from hydrocarbon-grown cells of *Cladosporium resinae*, 565
- Casida, L.E. Jr. *Arthrobacter* species as a prey cell reservoir for nonobligate bacterial predators in soil, 559
- Chadwick, J.S. see Dunphy, G.B., 508
- Chadwick, J.S. see Dunphy, G.B., 747
- Chalifour, F.-P., and Benhamou, N. Indirect evidence for cellulase production by *Rhizobium* in pea root nodules during bacteroid differentiation: cytochemical aspects of cellulose breakdown in rhizobial droplets, 821
- Chalutz, E. see Droby, S., 794
- Chamroux, S. see Corre, S., 740
- Chan, Y.-K., Barran, L.R., and Bromfield, E.S.P. Denitrification activity of phage types representative of two populations of indigenous *Rhizobium meliloti*, 737
- Charest, M. see Parrot, M., 366
- Charlebois, R.L., Hofman, J.D., Schalkwyk, L.C., Lam, W.L., and Doolittle, W.F. Genome mapping in halobacteria, 21
- Charlebois, R.L. see Cline, S.W., 148
- Charlton, K.M. see Webster, W.A., 811
- Cheng, K.-J., Phillippe, R.C., McLean, R.J.C., and Costerton, J.W. The characterization and ultrastructure of two new strains of *Butyrivibrio*, 274
- Cheng, K.-J. see Imai, S., 686
- Chisnell, J.R. see Premakumar, R., 344
- Chopra, A.K., and Houston, C.W. Purification and partial characterization of a cytotoxic enterotoxin produced by *Aeromonas hydrophila*, 719
- Cline, S.W., Lam, W.L., Charlebois, R.L., Schalkwyk, L.C., and Doolittle, W.F. Transformation methods for halophilic archaeobacteria, 148
- Conway, P.L. see Wrangstadh, M., 309
- Cooney, J.J. see Carson, D.B., 565
- Corre, S., Prieur, D., Chamroux, S., Floch, J.-Y., et Hourmant, A. Étude préliminaire de communautés bactériennes épiphytes de *Laminara digitata*, 740
- Costerton, J.W. see Cheng, K.-J., 274
- Crawford, D.L. see Wang, Z., 535
- Crawford, D.L. see Bleakley, B.H., 544
- Cumaraswamy, A., and Henney, H.R., Jr. Adenine salvage enzymes and intracellular nucleotide triphosphate content in *Physarum flavicomum* amoebae during growth and development, 554
- Cunningham, J. see Widden, P., 469
- Cuppels, D.A. see Moore, R.A., 910
- Dalton, M.T., and Bezanson, G.S. The isolation, from a prosthetic device site, of a rare bacterium belonging to CDC enteric group 58, 819
- Daneshvar, M.I. see Pine, L., 245
- Daneshvar, M.I., Brooks, J.B., Malcolm, G.B., and Pine, L. Analyses of fermentation products of *Listeria* species by frequency-pulsed electron-capture gas-liquid chromatography, 786
- Daniels, C.J. see Thompson, L.E., 36
- Daniels, L. see Mukhopadhyay, B., 499
- Danson, M.J. Central metabolism of the archaeobacteria: an overview, 58
- DasSarma, S. Mechanisms of genetic variability in *Halobacterium halobium*: the purple membrane and gas vesicle mutations, 65
- DasSarma, S. see Hackett, N.R., 86
- Datta, A. see Sasmal, D., 642
- Datta, P.K., Hawkins, L.K., and Gupta, R. Presence of an intron in elongator methionine-tRNA of *Halobacterium volcanii*, 189
- Dave, P. see Mody, R., 1022
- Davidson, B.E. see Powell, I.B., 860
- Davis, R.E. see Lee, I.-M., 1087
- Davis, R.E. see Lee, I.-M., 1092
- Dawood, M.R. see Jay, F.T., 334
- Debets, A.J.M., Swart, K., and Bos, C.J. Mitotic mapping in linkage group V of *Aspergillus niger* based on selection of auxotrophic recombinants by Novozym enrichment, 982
- De Boer, S.H. see Ward, L.J., 651
- Demain, A.L. see Zhang, J., 399
- De Mot, R., and Vanderleyden, J. Application of two-dimensional protein analysis for strain fingerprinting and mutant analysis of *Azospirillum* species, 960
- Dennis, P.P. Introduction, 1
- Dennis, P.P. see Shimmin, L.C., 164
- Dennis, P.P. see May, B.P., 171
- Dennis, P.P. see Ramirez, C., 234
- Dennis, P.P. see Ramirez, C., 975
- Derckacheva, N.I. see Kagramanova, V.K., 160
- de Roubin, M.-R., Mulligan, C.N., and Gibbs, B.F. Correlation of enhanced surfactin production with decreased isocitrate dehydrogenase activity, 854
- Deutch, C.E., Hasler, J.M., Houston, R.M., Sharma, M., and Stone, V.J. Nonspecific inhibition of proline dehydrogenase synthesis in *Escherichia coli* during osmotic stress, 779
- Dillon, J.R. see Picard, F.J., 1069
- Doig, P., Paranchych, W., Sastry, P.A., and Irvin, R.T. Human buccal epithelial cell receptors of *Pseudomonas aeruginosa*: identification of glycoproteins with pilus binding activity, 1141
- Doolittle, W.F. see Charlebois, R.L., 21
- Doolittle, W.F. see Cline, S.W., 148
- Doran, C.C. see Kadam, S.K., 646
- Doran, J.L. see Semple, K.M., 925
- Downing, W.L. see Shimmin, L.C., 164
- Droby, S., Chalutz, E., Wilson, C.L., and Wisniewski, M. Characterization of the biocontrol activity of *Debaryomyces hansenii* in the control of *Penicillium digitatum* on grapefruit, 794
- Dunphy, G.B., and Nolan, R.A. Development of *Entomophaga aulicae* protoplasts in synthetic eastern hemlock looper hemolymph, 304
- Dunphy, G.B., and Chadwick, J.S. Effects of selected carbohydrates and the contribution of the prophenoloxidase cascade system to the adhesion of strain of *Pseudomonas aeruginosa* and *Proteus mirabilis* to hemocytes of nonimmune larval *Galleria mellonella*, 508
- Dunphy, G.B., and Chadwick, J.S. Erratum: Effects of selected carbohydrates and the contribution of the prophenoloxidase cascade system to the adhesion of strains of *Pseudomonas aeruginosa* and *Proteus mirabilis* to hemocytes of nonimmune larval *Galleria mellonella*, 747
- Ehrhardt, J.C. see Boonkitticharoen, V., 874
- Elie, C. see Forterre, P., 228
- Erdmann, V.A. see Wolters, J., 43
- Fabry, S. see Hensel, R., 81
- Falkinham, J.O., III. see George, K.L., 529
- Ferris, F.G., Fyfe, W.S., Witten, T., Schultze, S., and Beveridge, T.J. Effect of mineral substrate hardness on the population density of epilithic microorganisms in two Ontario rivers, 744
- Finnerty, W.R. see Modrzakowski, M.C., 1031

- Floch, J.-Y. see Corre, S., 740
- Fonty, G., Gouet, P., and Nebout, J.M. Development of the cellulolytic microflora in the rumen of lambs transferred into sterile isolators a few days after birth, 416
- Fonty, G. see Rieu, F., 698
- Ford, E.J. see Miller, R.V., 517
- Forterre, P., Elie, C., Sioud, M., and Hamal, A. Studies on DNA polymerases and topoisomerases in archaeobacteria, 228
- Frank, H.A. see Ronning, I.E., 388
- Fredrickson, J.K., Bentjen, S.A., Bolton, H., Jr., Li, S.W., and Van Voris, P. Fate of Tn5 mutants of root growth-inhibiting *Pseudomonas* sp. in intact soil-core microcosms, 867
- Frey, G. see Thomm, M., 30
- Fuhrmann, B., Roquebert, M.F., Van Hoegaerden, M., and Strosberg, A.D. Immunological differentiation of *Penicillium* species, 1043
- Fukami, K. see Satoh, H., 329
- Fyfe, W.S. see Ferris, F.G., 744
- Gálvez, A., Valdivia, E., Martínez, M., and Maqueda, M. Bactericidal action of peptide antibiotic AS-48 against *Escherichia coli* K-12, 318
- Ganju, R.K., Vithayathil, P.J., and Murthy, S.K. Purification and characterization of two xylanases from *Chaetomium thermophile* var. *coprophile*, 836
- Garber, G.E., and Lemchuk-Favel, L.T. Characterization and purification of extracellular proteases of *Trichomonas vaginalis*, 903
- Garrett, R.A. see Zillig, W., 73
- Garrett, R.A. see Kjems, J., 210
- Gauthier, M.J., Munro, P.M., and Breittmayer, V.A. Influence of prior growth conditions of low nutrient response of *Escherichia coli* in seawater, 379
- Gauthier, M.J., Thomas, P., et Munro, P.M. Modification de la structure des enveloppes et du contenu en protéines d'*Escherichia coli* en survie dans l'eau de mer, 843
- George, K.L., and Falkinham, J.O., III. Identification of cytoplasmic membrane protein antigens of *Mycobacterium avium*, *M. intracellulare*, and *M. Scrofulaceum*, 529
- Gibbs, B.F. see de Roubin, M.-R., 854
- Gilewicz, M. see Bonin, P., 1061
- Giron, M.Y., and Morrell, J.J. Fungi colonizing preservative-treated Douglas-fir poles after remedial treatment with fumigants, 283
- Girones, R., Jofre, J.T., and Bosch, A. Isolation of marine bacteria with antiviral properties, 1015
- Goldman, R.C. see Kadam, S.K., 646
- Gong, C.S. see Tang, R.T., 668
- Goodwin, P.H. Cloning and expression of *Xylella fastidiosa* antigens in *Escherichia coli* and *Erwinia stewartii*, 487
- Goto, N. see Arimitsu, Y., 1009
- Gouet, P. see Fonty, G., 416
- Gouet, P. see Rieu, F., 698
- Gouet, P. see Brunel, A., 989
- Grenier, D. see Mayrand, D., 607
- Gropp, F. see Zillig, W., 73
- Gropp, F., Palm, P., and Zillig, W. Expression and regulation of *Halobacterium halobium* phage  $\Phi$ H genes, 182
- Guhathakurta, B. see Sasmal, D., 642
- Guinea, J. see Trias, J., 1037
- Gupta, K.G. see Prabha, V., 1076
- Gupta, M. see Prabha, V., 1076
- Gupta, R. see Datta, P.K., 189
- Gustafsson, K. Growth and survival of four strains of *Francisella tularensis* in a rich medium preconditioned with *Acanthamoeba palestinensis*, 1100
- Gyles, C.L. see MacLeod, D.L., 623
- Hackett, N.R., and DasSarma, S. Characterization of the small endogenous plasmid of *Halobacterium* strain SB3 and its use in transformation of *H. halobium*, 86
- Hadobas, P.A. see Trinick, M.J., 1156
- Hamal, A. see Forterre, P., 228
- Hamana, K., Akiba, T., Uchino, F., and Matsuzaki, S. Distribution of spermine in bacilli and lactic acid bacteria, 450
- Hammes, W. see König, H., 176
- Han, S.S. see Imai, S., 686
- Hartmann, H.J. see Marvalín, O., 706
- Hasler, J.M. see Deutch, C.E., 779
- Hatakeyama, T. see Kimura, M., 195
- Hatakeyama, T. see Kimura, M., 195
- Hawkins, L.K. see Datta, P.K., 189
- Hendrickson, O.Q. Implications of natural ethylene cyclin processes for forest soil acetylene reduction assays, 713
- Henken, G. see Miller, H.J., 656
- Henney, H.R., Jr. see Cumaraswamy, A., 554
- Hensel, R., Zwickl, P., Fabry, S., Lang, J., and Palm, P. Sequence comparison of glyceraldehyde-3-phosphate dehydrogenases from the three eukaryotes: evolutionary implication, 81
- Higgins, V.J. see Butler, M.J., 728
- Hildebrand, A. see Lämmle, C., 614
- Hillier, A.J. see Powell, I.B., 860
- Hofman, J.D. see Charlebois, R.L., 21
- Honek, J.F. see Wright, G.D., 945
- Horgen, P.A., Kokurewicz, K.F., and Anderson, J.B. The germination of basidiospores from commercial and wild-collected isolates of *Agaricus bisporus* (= *A. brunneus*), 492
- Horgen, P.A. see Horton, J.S., 1146
- Horne, M. see Pfeifer, F., 96
- Horton, J.S., and Horgen, P.A. Polymorphisms in the nuclear DNA of *Achlya* species: some taxonomic implications, 1146
- Hourmant, A. see Corre, S., 740
- Houston, C.W. see Chopra, A.K., 719
- Houston, R.M. see Deutch, C.E., 779
- Hurst, C.J., Benton, W.H., and McClellan, K.A. Thermal and water source effects upon the stability of enteroviruses in surface freshwaters, 474
- Hynes, M.F. see Kucey, R.M.N., 661
- Imai, S., Han, S.S., Cheng, K.-J., and Kudo, H. Composition of the rumen ciliate population in experimental herds of cattle and sheep in Lethbridge, Alberta, Western Canada, 686
- Inoue, Y. see Murata, K., 423
- Irvin, R.T. see Doig, P., 1141
- Ishiguro, E.E. see Tao, J.-S., 1051
- Jay, F.T., Dawood, M.R., and Luk, S.K.S. Infectivity-deficient vesicular stomatitis virus produced in the presence of interferon has a functional virion core, 334
- Jensen, B.K. ATP-related specific heterotrophic activity in petroleum contaminated and uncontaminated groundwaters, 814
- Jensen, J. see Kjems, J., 210
- Jensen, S.E. see Rollins, M.J., 1111
- Jofre, J.T. see Girones, R., 1015
- Johnson, B.F., Sowden, L.C., Walker T., Yoo, B.Y., and Calleja, G.B. Use of electron microscopy to characterize the surfaces of flocculent and nonflocculent yeast cells, 1081
- Kadam, S.K., Doran, C.C., and Goldman, R.C. Accumulation of incomplete metabolic side products of lipid A in *Salmonella typhimurium* during inhibition of 3-deoxy-D-manno-

- oculosonate incorporation by a new class of antibacterial agents, 646
- Kagramanova, V.K. see Spiridonova, V.A., 153
- Kagramanova, V.K., Derkacheva, N.I., and Mankin, A.S. Unusual nucleotide sequence heterogeneity of small multicopy pHSB plasmid from *Halobacterium* strain SB3, an archaeobacterium 160
- Kandler, O. see König, H., 176
- Kanno, S. see Kumakura, M., 968
- Kimura, A. see Murata, K., 423
- Kimura, J. see Kimura, M., 195
- Kimura, M., Arndt, E., Hatakeyama, T., Hatakeyama, T., and Kimura, J. Ribosomal proteins in halobacteria, 195
- Kirchner, P.T. see Boonkitticharoen, V., 874
- Kjelleberg, S. see Wrangstadh, M., 309
- Kjems, J., Jensen, J., Olesen, T., and Garrett, R.A. Comparison of transfer RNA and ribosomal RNA intron splicing in the extreme thermophile and archaeobacterium *Desulfurococcus mobilis*, 210
- Klein, A. see Allmansberger, R., 52
- Klenk, H.-P. see Zillig, W., 73
- Koch, A.L. Erratum: Why can't a cell grow infinitely fast?, 605
- Kokurewicz, K.F. see Horgen, P.A., 492
- König, H., Kandler, O., and Hammes, W. Biosynthesis of pseudomurein: isolation of putative precursors from *Methanobacterium thermoautotrophicum*, 176
- Köpke A.K.E., and Wittmann-Liebold, B. Comparative studies of ribosomal proteins and their genes from *Methanococcus vannielii* and other organisms, 11
- Köpke, A.K.E. see Spiridonova, V.A., 153
- Krishnamurthy, S. see Mody, R., 1022
- Kröckel, L. see Allmansberger, R., 52
- Kropinski, A.M.B. see Bigby, D., 630
- Kucey, R.M.N., and Hynes, M.F. Populations of *Rhizobium leguminosarum* biovars *phaseoli* and *viciae* in fields after bean or pea in rotation with nonlegumes, 661
- Kudo, H. see Imai, S., 686
- Kumakura, M., Kanno, S., and Nisizawa, K. Cellulase production in *Trichoderma reesei* immobilized with polymeric fibrous carriers, 968
- Laakso, D.H. see McCallum, K.L., 994
- Lachance, M.-A. see Butler, M.J., 728
- Laishley, E.J. see Bryant, R.D., 481
- Lake, J.A. Origin of the eukaryotic nucleus: eukaryotes and eocytes are genotypically related, 109
- Lam, W.L. see Charlebois, R.L., 21
- Lam, W.L. see Cline, S.W., 148
- Lamarre, A., and Talbot, P.J. Effect of pH and temperature on the infectivity of human coronavirus 229E, 972
- Lämmier, C., Alaboudi, A., and Hildebrand, A. Characterization of albumin-binding properties of *Peptostreptococcus magnus*, 614
- Lang, J. see Hensel, R., 81
- Lavoie, M.C. see Parrot, M., 366
- Lawton, P., Whitaker, A., Odell, D., and Stowell, J.D. Actinomycete morphology in shaken culture, 881
- Lazarek, S. see Marvalín, O., 706
- Lazarovits, G. see Butler, M.J., 728
- Lechner, K. see Auer, J., 200
- Leclerc, D., and Asselin, A. Detection of bacterial cell wall hydrolases after denaturing polyacrylamide gel electrophoresis, 749
- Lecomte, J. see Payment, P., 550
- Lee, B.C. see Schryvers, A.B., 404
- Lee, I.-M., and Davis, R.E. Defects of helicity and motility in the corn stunt spiroplasma, *Spiroplasma kunkelii*, 1087
- Lee, I.-M., and Davis, R.E. Serum-free media for cultivation of spiroplasmas, 1092
- Lefebvre, G.M. see Bédard, J., 760
- Leffers, H. see Zillig, W., 73
- Lemchuk-Favel, L.T. see Garber, G.E., 903
- Leong, D.M. see Betlach, M.C., 134
- Letarte, R. see Valéro, J.R., 444
- Levanony, H. see Bashan, Y., 691
- Levanony, H. see Bashan, Y., 936
- Levine, W.B., and Marzluf, G.A. Isolation and characterization of cadmium-resistant mutants of *Neurospora crassa*, 359
- Li, S.W. see Fredrickson, J.K., 867
- Loewen, P.C. Genetic mapping of *katB*, a locus that affects catalase 2 levels in *Bacillus subtilis*, 807
- Lopez, M.F. see Murry, M.A., 636
- Lorén, J.G. see Trias, J., 1037
- Louie, A. see Shimmin, L.C., 164
- Luk, S.K.S. see Jay, F.T., 334
- Ma, S.-W. see Moore, R.A., 910
- MacLeod, D.L., and Gyles, C.L. Effects of culture conditions on yield of Shiga-like toxin-IIv from *Escherichia coli*, 623
- Mailhot, K. see Sylvestre, M., 439
- Malcolm, G.B. see Pine, L., 245
- Malcolm, G.B. see Daneshvar, M.I., 786
- Mankin, A.S. see Spiridonova, V.A., 153
- Mankin, A.S. see Kagramanova, V.K., 160
- Mann-Dean, M.G. see Wales, M.E., 432
- Maqueda, M. see Gálvez, A., 318
- Marín, I. see Amils, R., 141
- Martínez, M. see Gálvez, A., 318
- Marvalín, O., Aleya, L., Hartmann, H.J., and Lazarek, S. Coupling of the seasonal patterns of bacterioplankton and phytoplankton in a eutrophic lake, 706
- Marzluf, G.A. see Levine, W.B., 359
- Massé, R. see Sylvestre, M., 439
- Matheson, A.T. see Shimmin, L.C., 164
- Matheson, A.T. see Ramirez, C., 234
- Matheson, A.T. see Ramirez, C., 975
- Matsuzaki, S. see Hamana, K., 450
- May, B.P., Tam, P., and Dennis, P.P. The expression of the superoxide dismutase gene in *Halobacterium cutirubrum* and *Halobacterium volcanii*, 171
- Mayers, I.T., and Beveridge, T.J. The sorption of metals to *Bacillus subtilis* walls from dilute solutions and simulated Hamilton Harbour (Lake Ontario) water, 764
- Mayrand, D., and Grenier, D. Biological activities of outer membrane vesicles, 607
- McCallum, K.L., Laakso, D.H., and Whitfield, C. Use of a bacteriophage-encoded glycanase enzyme in the generation of lipopolysaccharide O side chain deficient mutants of *Escherichia coli* O9:K30 and *Klebsiella* O1:K20: role of O and K antigens in resistance to complement-mediated serum killing, 994
- McClellan, K.A. see Hurst, C.J., 474
- McFeters, G.A. see Pyle, B.H., 520
- McLean, R.J.C. see Cheng, K.-J., 274
- Merkel, G.J., and Phelps, C.L. The effects of amphotericin B on the interaction of *Candida albicans* with fibroblasts cultures, 255
- Merkel, G.J., and Phelps, C.L. Conditions affecting the amphotericin B mediated inhibition of *Candida albicans*



- attachment to cell cultures, 260
- Mevarech, M. see Rosenshine I., 92
- Miller, H.J., Henken, G., and van Veen, J.A. Variation and composition of bacterial populations in the rhizospheres of maize, wheat, and grass cultivars, 656
- Miller, R.D. see Bortner, C.A., 1048
- Miller, R.V., Ford, E.J., and Sands, D.C. A nonsclerotial pathogenic mutant of *Sclerotinia sclerotiorum*, 517
- Mitiku, G. see Bashan, Y., 691
- Modrzakowski, M.C., and Finnerty, W.R. Intermediary metabolism of *Acinetobacter* grown on diakyl ethers, 1031
- Mody, R., Krishnamurthy, S., and Dave, P. Influence of far-ultraviolet radiation on the permeability of the outer membrane of *Escherichia coli*, 1022
- Montie, T.C. see Anderson, T.R., 890
- Moore, R.A., Starratt, A.N., Ma, S.-W., Morris, V.L., and Cuppels, D.A. Identification of a chromosomal region required for biosynthesis of the phytotoxin coronatine by *Pseudomonas syringae* pv. *tomato*, 910
- Moribayashi, A. see Arimitsu, Y., 1009
- Mormile, M.R., and Atlas, R.M. Biotransformation of dibenzothiophene to dibenzothiophene sulfone by *Pseudomonas putida*, 603
- Morrell, J.J. see Giron, M.Y., 283
- Morris, V.L. see Moore, R.A., 910
- Mukhopadhyay, B., and Daniels, L. Aerobic purification of  $N^5, N^{10}$ -methylenetetrahydromethanopterin dehydrogenase, separated from  $N^5, N^{10}$ -methenyltetrahydromethanopterin cyclohydrolase, from *Methanobacterium thermoautotrophicum* strain Marburg, 499
- Mukohata, Y. see Tanaka, M., 524
- Mukohata, Y. see Tanaka, M., 748
- Mullen, M.D., and Wollum, A.G., II. Variation among different cultures of *Bradyrhizobium japonicum* strains USDA 110 and 122, 583
- Mulligan, C.N. see de Roubin, M.-R., 854
- Munro, P.M. see Gauthier, M.J., 379
- Munro, P.M. see Gauthier, M.J., 843
- Murata, K., Inoue, Y., Rhee, H.-i., and Kimura, A. 2-Oxo-aldehyde metabolism in microorganisms, 423
- Murry, M.A., and Lopez, M.F. Interaction between hydrogenase, nitrogenase, and respiratory activities in a *Frankia* isolate from *Alnus rubra*, 636
- Murthy, S.K. see Ganju, R.K., 836
- Nahas, E. Control and localization of the phosphatases in conidia of *Neurospora crassa*, 830
- Nájera, R. see Soberón-Chávez, G., 464
- Nath, S.K. Invasion of HeLa cells by  $\beta$ -hemolytic group G streptococci, 515
- Nebout, J.M. see Fonty, G., 416
- Newton, C.H. see Shimmin, L.C., 164
- Newton, C.H. see Ramirez, C., 234
- Newton, C.H. see Ramirez, C., 975
- Nieuwlandt, D.T. see Thompson, L.D., 36
- Nisizawa, K. see Kumakura, M., 968
- Nolan, R.A. see Dunphy, G.B., 304
- Nolan, R.A. Stage-specific changes in cytoplasmic protein synthesis in *Entomophaga aulicae* protoplasts, 373
- Nowak, J., and Tsai, H. Purification and properties of three endopeptidases from baker's yeast, 295
- Odell, D. see Lawton, P., 881
- Oesterheld, D. see Soppa, J., 205
- Olesen, T. see Kjems, J., 210
- Olsen, G.J., and Woese, C.R. A brief note concerning archaeobacterial phylogeny, 119
- Pacovsky, R.S. Diazotroph establishment and maintenance in the *Sorghum-Glomus-Azospirillum* association, 977
- Palm, P. see Zillig, W., 73
- Palm, P. see Hensel, R., 81
- Palm, P. see Gropp, F., 182
- Paranchych, W. see Doig, P., 1141
- Parrot, M., Charest, M., and Lavoie, M.C. Production of mutacin-like substances by *Streptococcus mutans*, 366
- Paul, J.W., Beauchamp, E.G., and Trevors, J.T. Acetate, propionate, butyrate, glucose, and sucrose as carbon sources for denitrifying bacteria in soil, 754
- Payment, P., Trudel, M., Thibodeau, L., and Lecomte, J. Production and characterization of neutralizing monoclonal antibodies against poliovirus type 1, 2, and 3, 550
- Payment, P., Bérubé, A., Perreault, D., Armon, R., and Trudel, M. Concentration of *Giardia lamblia* cysts. *Legionella pneumophila*, *Clostridium perfringens*, human enteric viruses, and coliphages from large volumes of drinking water, using a single filtration, 932
- Payment, P. Bacterial colonization of domestic reverse-osmosis water filtration units, 1065
- Pažout, J., and Pažoutová, S. Ethylene is synthesized by vegetative mycelium in surface cultures of *Penicillium cyclopium* Westling, 384
- Pažout, J., and Pažoutová, S. Relationship between aeration, carbon source, and respiration yield and the ethylene production and differentiation of static cultures of *Penicillium cyclopium* and *P. velutinum*, 619
- Pažoutová, S. see Pažout, J., 384
- Pažoutová, S. see Pažout, J., 619
- Penner, J.L. see Preston, M.A., 265
- Perreault, D. see Payment, P., 932
- Peterson, J.B. The use of metronidazole to study pyridine nucleotide reduction *in vivo* in *Azotobacter vinelandii*, 340
- Peterson, J.B. Respiratory differences associated with culture aeration in *Azotobacter vinelandii*, 918
- Pfeifer, F., Blaseio, U., and Horne, M. Genome structure of *Halobacterium halobium*: plasmid dynamics in gas vacuole deficient mutants, 96
- Phelps, C.L. see Merkel, G.J., 255
- Phelps, C.L. see Merkel, G.J., 260
- Phillippe, R.C. see Cheng, K.-J., 274
- Phillips, A.J.L. Relationships of *Rhizoctonia solani* inoculum density to incidence of hypocotyl rot and damping-off in dry beans, 1132
- Phipps, B.M. see Baumeister, W., 215
- Picard, F.J., and Dillon, J.R. Biochemical and genetic studies with arginine and proline auxotrophs of *Neisseria gonorrhoeae*, 1069
- Pine, L., Malcolm, G.B., Brooks, J.B., and Daneshvar, M.I. Physiological studies on the growth and utilization of sugars by *Listeria* species, 245
- Pine, L. see Daneshvar, M.I., 786
- Pisabarro, A.G. see Amils, R., 141
- Pomatto, A.L., III. see Wang, Z., 535
- Powell, I.B., Arnold, P.M., Hillier, A.J., and Davidson, B.E. Molecular comparison of prolate- and isometric-headed bacteriophages of lactococci, 860
- Prabha, V., Gupta, M., and Gupta, K.G. Kinetic properties of  $7\alpha$ -hydroxysteroid dehydrogenase from *Escherichia coli* 080, 1076

- Premakumar, R., Chisnell, J.R., and Bishop, P.E. A comparison of the three dinitrogenase reductases expressed by *Azotobacter vinelandii*, 344
- Preston, M.A., and Penner, J.L. Characterization of cross-reacting serotypes of *Campylobacter jejuni*, 265
- Prieur, D. see Corre, S., 740
- Pühler, G. see Zillig, W., 73
- Pyle, B.H., and McFeters, G.A. Iodine sensitivity of bacteria isolated from iodinated water systems, 520
- Quiot, J.M. see Vey, A., 1000
- Rafii, F. see Wang, Z., 535
- Ramagopal, S. Synthesis of a ribosome-bound translatable poly(A)<sup>-</sup> mRNA during spore germination in *Dictyostelium discoideum*, 573
- Ramagopal, S. Unequal accumulation of 26S and 17S RNAs in ribosomes during spore germination in *Dictyostelium discoideum*, 850
- Ramanand, K. see Sharmila, M., 1105
- Ramirez, C. see Shimmin, L.C., 164
- Ramirez, C., Shimmin, L.C., Newton, C.H., Matheson, A.T., and Dennis, P.P. Structure and evolution of the L11, L1, L10, and L12 equivalent ribosomal proteins in eubacteria, archaeobacteria, and eucaryotes, 234
- Ramirez, C., Shimmin, L.C., Newton, C.H., Matheson, A.T., and Dennis, P.P. Erratum: Structure and evolution of the L11, L1, L10, and L12 equivalent ribosomal proteins in eubacteria, archaeobacteria, and eucaryotes, 975
- Ramirez, L. see Amils, R., 141
- Ree, H.K., Cao, K., Thurlow, D.L., and Zimmermann, R.A. The structure and organization of the 16S ribosomal RNA gene from the archaeobacterium *Thermoplasma acidophilum*, 124
- Reeve, J.N. see Weil, C.F., 101
- Regué, M. see Camprubí, S., 735
- Rhee, H.-i. see Murata, K., 423
- Richter, D.L., and Bruhn, J.N. Revival of saprotrophic and mycorrhizal basidiomycete cultures from cold storage in sterile water, 1055
- Rieu, F., Fonty, G., and Gouet, P. Colony counts and characterization of bacteria adherent to the rumen wall and desquamated epithelial cells in conventional young lambs, 698
- Rollins, M.J., Jensen, S.E., and Westlake, D.W.S. Isopenicillin N synthase and desacetoxycephalosporin C synthase activities during defined medium fermentations of *Streptomyces clavuligerus*: effect of oxygen and iron supplements, 1111
- Ronning, I.E., and Frank, H.A. Morphological changes in putrefactive anaerobe 3679 (*Clostridium sporogenes*) induced by sorbate, hydrochloric acid, and nitrite, 388
- Roquebert, M.F. see Fuhrmann, B., 1043
- Rosenshine, I., and Mevarech, M. Isolation and partial characterization of plasmids found in three *Halobacterium volcanii* isolates, 92
- Roussard-Jacquemin, M. Effets de la carence en sodium sur la cytologie de la cyanobactérie *Anabaena cylindrica* Lemm, 322
- Sanangelantoni, A.M. see Cammarano, P., 2
- Sands, D.C. see Miller, R.V., 517
- Sanz, J.L. see Amils, R., 141
- Sasmal, D., Guhathakurta, B., Sikdar, S.N., and Datta, A. Factors affecting the colonization of isolated rabbit intestinal epithelial cells by *Vibrio cholerae* 01 *in vitro*, 642
- Sastry, P.A. see Doig, P., 1141
- Sato, H., Fukami, K., Watanabe, K., and Takahashi, E. Seasonal changes in heterotrophic bacteria under fast ice near Syowa station, Antarctica, 329
- Saucedo, J.E.N., Barbotin, J.-N., Velut, M., and Thomas, D. Ultrastructural examination of *Gibberella fujikuroi* mycelia: effect of immobilization in calcium alginate beads, 1118
- Sayler, G.S. see Steffan, R.J., 681
- Sayre, R.M., and Wergin, W.P. Morphology and fine structure of the trophozoites of *Theratomyxa weberi* (Protozoa: Vampyrellidae) predacious on soil nematodes, 589
- Schalkwyk, L.C. see Charlebois, R.L., 21
- Schalkwyk, L.C. see Cline, S.W., 148
- Schallenberg, J. see Allmansberger, R., 52
- Schippers, B. see van Peer, R., 456
- Schryvers, A.B., and Lee, B.C. Comparative analysis of the transferrin and lactoferrin binding proteins in the family *Neisseriaceae*, 404
- Schultze, S. see Ferris, F.G., 744
- Semple, K.M., Doran, J.L., and Westlake, D.W.S. DNA relatedness of oil-field isolates of *Shewanella putrefaciens*, 925
- Sethunathan, N. see Sharmila, M., 1105
- Shand, R.F. see Betlach, M.C., 134
- Sharma, M. see Deutch, C.E., 779
- Sharmila, M., Ramanand, K., and Sethunathan, N. Effect of yeast extract on the degradation of organophosphorus insecticides by soil enrichment and bacterial cultures, 1105
- Sherf, B.A. see Thomm, M., 30
- Sherf, B.A. see Weil, C.F., 101
- Shimmin, L.C., Newton, C.H., Ramirez, C., Yee, J., Downing, W.L., Louie, A., Matheson, A.T., and Dennis, P.P. Organization of genes encoding the L11, L1, L10, and L12 equivalent ribosomal proteins in eubacteria, archaeobacteria, and eucaryotes, 164
- Shimmin, L.C. see Ramirez, C., 234
- Shimmin, L.C. see Ramirez, C., 975
- Sikdar, S.N. see Sasmal, D., 642
- Sinclair, J.L., and Alexander, M. Effect of protozoan predation on relative abundance of fast- and slow-growing bacteria, 578
- Sioud, M. see Forterre, P., 228
- Soberón-Chávez, G., and Nájera, R. Isolation from soil of *Rhizobium leguminosarum* lacking symbiotic information, 464
- Soppa, J., and Oesterhelt, D. *Halobacterium* sp. GRB: a species to work with!?, 205
- Sowden, L.C. see Johnson, B.F., 1081
- Spiridonova, V.A., Akhmanova, A.S., Kagramanova, V.K., Köpke, A.K.E., and Mankin, A.S. Ribosomal protein gene cluster of *Halobacterium halobium*: nucleotide sequence of the genes coding for S3 and L29 equivalent ribosomal proteins, 153
- Starodub, M.E. see Trevors, J.T., 675
- Starodub, M.E. see van Elsas, J.D., 951
- Starodub, M.E. see Trevors, J.T., 975
- Starratt, A.N. see Moore, R.A., 910
- Steffan, R.J., Breen, A., Atlas, R.M., and Sayler, G.S. Application of gene probe methods for monitoring specific microbial populations in freshwater ecosystems, 681
- Stelmaschuk, S. see von Tigerstrom, R.G., 511
- Stone, V.J. see Deutch, C.E., 779
- Stowell, J.D. see Lawton, P., 881
- Strosberg, A.D. see Fuhrmann, B., 1043
- Sugii, S., and Tsuji, T. Binding specificities of heat-labile enterotoxins isolated from porcine and human enterotoxigenic *Escherichia coli* for different gangliosides, 670
- Swart, K. see Debets, A.J.M., 982
- Sylvestre, M., Mailhot, K., Ahmad, D., and Massé, R. Isolation and preliminary characterization of a 2-chlorobenzoate degrading *Pseudomonas*, 439

- Takahashi, E. see Satoh, H., 329
- Talbot, P.J. see Lamarre, A., 972
- Tam, P. see May, B.P., 171
- Tanaka, M., Mukohata, Y., and Yuasa, S. Utilization of D-amino acids by *Halobacterium halobium* R<sub>1</sub>mR<sup>1</sup>, 524
- Tanaka, M., Mukohata, Y., and Yuasa, S. Erratum: Utilization of D-amino acids by *Halobacterium halobium* R<sub>1</sub>mR<sup>1</sup>, 748
- Tang, R.T., Zhu, X.Z., and Gong, C.S. Effect of dimethyl sulfoxide on L-lysine production by a regulatory mutant of *Brevibacterium flavum*, 668
- Tao, J.-S., and Ishiguro, E.E. Nucleotide sequence of the *murE* gene of *Escherichia coli*, 1051
- Taylor, D.E. see Yan, W., 289
- Thibodeau, L. see Payment, P., 550
- Thomas, D. see Saucedo, J.E.N., 1118
- Thomas, P. see Gauthier, M.J., 843
- Thomm, M., Wich, G., Brown, J.W., Frey, G., Sherf, B.A., and Beckler, G.S. An archaeobacterial promoter sequence assigned by RNA polymerase binding experiments, 30
- Thompson, L.D., Brandon, L.D., Nieuwlandt, D.T., and Daniels, C.J. Transfer RNA intron processing in the helophilic archaeobacteria, 36
- Thurlow, D.L. see Ree, H.K., 124
- Tiboni, O. see Cammarano, P., 2
- Tomás, J. see Camprubí, S., 735
- Torrella, F. see Amat, A.S., 771
- Torrey, J.G. see Tzean, S.S., 801
- Trevors, J.T., van Elsas, J.D., Starodub, M.E., and Van Overbeek, L.S. Survival of and plasmid stability in *Pseudomonas* and *Klebsiella* spp. introduced into agricultural drainage water, 675
- Trevors, J.T. see Paul, J.W., 754
- Trevors, J.T., and van Elsas, J.D. A review of selected methods in environmental microbial genetics, 895
- Trevors, J.T. see van Elsas, J.D., 951
- Trevors, J.T., van Elsas, J.D., Starodub, M.E., and Van Overbeek, L.S. Erratum: Survival of and plasmid stability in *Pseudomonas* and *Klebsiella* spp. introduced into agricultural drainage water, 975
- Trias, J., Viñas, M., Guinea, J., and Lorén, J.G. Brown pigmentation in *Serratia marcescens* cultures associated with tyrosine metabolism, 1037
- Trinick, M.J., and Hadobas, P.A. Effectiveness and competition for nodulation of *Vigna unguiculata* and *Macroptilium atropurpureum* with *Bradyrhizobium* from *Parasponia*, 1156
- Trudel, M. see Payment, P., 550
- Trudel, M. see Payment, P., 932
- Tsai, H. see Nowak, J., 295
- Tsuji, T. see Sugii, S., 670
- Tzean, S.S., and Torrey, J.G. Spore germination and the life cycle of *Frankia* in vitro, 801
- Uchino, F. see Hamana, K., 450
- Ureña, D. see Amils, R., 141
- Valdivia, E. see Gálvez, A., 318
- Valéro, J.R., et Letarte, R. Diagnostic biochimique de la présence d'une intoxication par *Bacillus thuringiensis* sérotype "H3a,3b" chez deux lépidoptères, 444
- Vanderleyden, J. see De Mot, R., 960
- van Elsas, J.D. see Trevors, J.T., 675
- van Elsas, J.D. see Trevors, J.T., 895
- van Elsas, J.D., Trevors, J.T., Van Overbeek, L.S., and Starodub, M.E. Survival of *Pseudomonas fluorescens* containing plasmids RP4 or pRK2501 and plasmid stability after introduction into two soils of different texture, 951
- van Elsas, J.D. see Trevors, J.T., 975
- Van Hoegaerden, M. see Fuhrmann, B., 1043
- Van Overbeek, L.S. see Trevors, J.T., 675
- Van Overbeek, L.S. see van Elsas, J.D., 951
- Van Overbeek, L.S. see Trevors, J.T., 975
- van Peer, R., and Schippers, B. Plant growth responses to bacterization with selected *Pseudomonas* spp. strains and rhizosphere microbial development in hydroponic cultures, 456
- van Veen, J.A. see Miller, H.J., 656
- Van Voris, P. see Fredrickson, J.K., 867
- Velut, M. see Saucedo, J.E.N., 1118
- Vey, A., et Quiot, J.M. Effet cytotoxique in vitro et chez l'insecte hôte des destruxines, toxines cyclodépsipeptidiques produites par le champignon entomopathogène *Metarhizium anisopliae*, 1000
- Viñas, M. see Trias, J., 1037
- Vithayathil, P.J. see Ganju, R.K., 836
- von Tigerstrom, R.G., and Stelmachuk, S. The use of Tween 20 in a sensitive turbidimetric assay of lipolytic enzymes, 511
- Wales, M.E., Mann-Dean, M.G., and Wild, J.R. Characterization of pyrimidine metabolism in the cellular slime mold, *Dictyostelium discoideum*, 432
- Walker, T. see Johnson, B.F., 1081
- Wang, Z., Crawford, D.L., Pometto, A.L., III, and Rafii, F. Survival and effects of wild-type, mutant, and recombinant *Streptomyces* in a soil ecosystem, 535
- Ward, L.J., and De Boer, S.H. Characterization of a monoclonal antibody against active pectate lyase from *Erwinia carotovora*, 651
- Watanabe, K. see Satoh, H., 329
- Webster, W.A., and Charlton, K.M. The apparent infection of NA-C1300 cell cultures by nucleocapsid material of the Canadian Arctic strain of rabies virus, 811
- Weil, C.F., Sherf, B.A., and Reeve, J.N. A comparison of the methyl reductase genes and gene products, 101
- Wergin, W.P. see Sayre, R.M., 589
- Westlake, D.W.S. see Semple, K.M., 925
- Westlake, D.W.S. see Rollins, M.J., 1111
- Whitaker, A. see Lawton, P., 881
- Whitfield, C. see McCallum, K.L., 994
- Wich, G. see Thomm, M., 30
- Widden, P., Cunningham, J., and Breil, B. Decomposition of cotton by *Trichoderma* species: influence of temperature, soil type, and nitrogen levels, 469
- Wild, J.R. see Wales, M.E., 432
- Wildhaber, I. see Baumeister, W., 215
- Wilson, C.L. see Droby, S., 794
- Wisniewski, M. see Droby, S., 794
- Witten, T. see Ferris, F.G., 744
- Wittmann-Liebold, B. see Köpke, A.K.E., 11
- Woese, C.R. see Olsen, G.J., 119
- Wolfe, S. see Zhang, J., 399
- Wollum, A.G., II. see Mullen, M.D., 583
- Wolters, J., and Erdmann, V.A. The structure and evolution of archaeobacterial ribosomal RNAs, 43
- Wrangstadh, M., Conway, P.L., and Kjelleberg, S. The role of an extracellular polysaccharide produced by the marine *Pseudomonas* sp. S9 in cellular detachment during starvation, 309
- Wright, G.D., and Honek, J.F. Effects of iron binding agents on *Saccharomyces cerevisiae* growth and cytochrome P450 content, 945
- Yan, W., and Taylor, D.E. Mapping of transfer and H pilus

- coding regions of the IncHII plasmid pHH1508a, 289
- Yee, J.** see Shimmin, L.C., 164
- Yoo, B.Y.** see Johnson, B.F., 1081
- You, C., and Zhou, F.** Non-nodular endorhizospheric nitrogen fixation in wetland rice, 403
- Yuasa, S.** see Tanaka, M., 524
- Yuasa, S.** see Tanaka, M., 748
- Zhang, J., Wolfe, S., and Demain, A.L.** Ammonium ions repress  $\delta$ -(L- $\alpha$ -aminoadipyl)-L-cysteinyl-D-valine synthetase in *Streptomyces clavuligerus* NRRL 3585, 399
- Zhou, F.** see You, C., 403
- Zhu, X.Z.** see Tang, R.T., 668
- Zillig, W., Klenk, H.-P., Palm, P., Pühler, G., Gropp, F., Garrett, R.A., and Leffers, H.** The phylogenetic relations of DNA-dependent RNA polymerases of archaeobacteria, eukaryotes, and eubacteria, 73
- Zillig, W.** see Gropp, F., 182
- Zimmermann, R.A.** see Ree, H.K., 124
- Zwickl, P.** see Hensel, R., 81



SUBJECT INDEX/INDEX DES MATIÈRES

- Acanthamoeba palestinensis* Francisella tularensis growth survival 1100  
Acetylene redn assay carbon monoxide 713  
Acetylglucosamine Vibrio adhesion intestine cell 642  
Achlya rRNA gene polymorphism 1146  
Acid phosphatase conidia Neurospora 830  
Acinetobacter alkyl ether dicarboxylate metab 1031  
Actinomyces morphol shaken culture 881  
Adenine phosphoribosyltransferase Physarum 554  
Adenosine phosphorylase Physarum 554  
Adhesion detachment Pseudomonas polysaccharide 309  
Adhesion hemocyte Pseudomonas Proteus carbohydrate 524  
Adhesion Vibrio intestine cell calcium acetylglucosamine 642  
Adsorption Azospirillum root hair 936  
Aeration Azotobacter respiration 918  
Aeromonas enterotoxin purifn characterization 719  
Agaricus bisporus germination basidiospore 492  
Alanine inosine Bacillus glucose triggering spore 760  
Albumin binding Peptostreptococcus 614  
Alcaligenes rice nitrogen fixation 403  
Alfalfa Rhizobium denitrification 737  
Alginate calcium Gibberella fujikuroi mycelia immobilization 1118  
Alk phosphatase conidia Neurospora 830  
Alkyl ether metab Acinetobacter 1031  
Amine Listeria metabolite 786  
Amino acid metab Halobacterium 508  
Amino acid metab Halobacterium correction 748  
Ammonium repression cephalosporin synthetase Streptomyces 399  
Amphotericin B Candida adhesion cell 260  
Amphotericin B Candida infection fibroblast 255  
Anabaena cytol sodium deficiency 322  
Anaerobic intestinal bacteria methanol inhibition 313  
Antibiotic AS48 sensitivity Escherichia 318  
Antibody flagella opsonophagocytosis Pseudomonas 890  
Antibody monoclonal pectate lyase Erwinia 651  
Antibody monoclonal poliovirus 550  
Antigen cytoplasmic membrane Mycobacterium 529  
Antigen gene Xylella cloning 487  
Antigen O K bacteria complement killing 994  
Antigen O lipopolysaccharide Klebsiella transformation 735  
Antigen variation Campylobacter cross reacting serotype 265  
Antiviral property marine bacteria isolation 1015  
Aplysia depilans galacturonic acid distribution fungi 349  
Archaeobacteria DNA polymerase topoisomerase review 228  
Archaeobacteria elongation factor Tu evolution 2  
Archaeobacteria evolution 119  
Archaeobacteria evolution ribosome 141  
Archaeobacteria glyceroldehyde phosphate dehydrogenase eubacteria eukaryote 81  
Archaeobacteria halophilic tRNA intron processing endonuclease 36  
Archaeobacteria metab review 58  
Archaeobacteria methanogenic gene mcr conservation 52  
Archaeobacteria promoter sequence detn 30  
Archaeobacteria RNA polymerase evolution eubacteria eukaryote 73  
Archaeobacteria surface protein organization review 215  
Archaeobacteria 5S rRNA structure evolution 43  
Arginine proline auxotroph Neisseria 1069  
Arthrobacter prey cell bacterial predator soil 559  
Aspergillus gene mapping Novozym enrichment 982  
ATP GTP Physarum growth development 554  
Azoferredoxin multiple form Azotobacter 344  
Azospirillum adsorption root hair 936  
Azospirillum proton efflux wheat root 691  
Azospirillum Sorghum Glomus diazotroph establishment maintenance 977  
Azospirillum strain fingerprinting mutant protein 960  
Azotobacter aeration respiration 918  
Azotobacter dinitrogenase reductase multiple form 344  
Azotobacter flavin redn metronidazole 340  
Bacillus alanine inosine glucose triggering spore 760  
Bacillus cell wall metal sorption 764  
Bacillus diagnosis lepidopteran cation 444  
Bacillus gene katB catalase mapping 807  
Bacillus spermine 450  
Bacillus surfactin fermn isocitrate dehydrogenase 854  
Bacteria abundance protozoan predation 578  
Bacteria anaerobic intestinal methanol inhibition 313  
Bacteria bone biochem taxonomy 819  
Bacteria colonization reverse osmosis water filtration 1065  
Bacteria denitrification soil carbon nutrition 754  
Bacteria heterotrophic groundwater petroleum product 814  
Bacteria hydrolase detection cell wall PAGE 749  
Bacteria iodine sensitivity 520  
Bacteria lactate spermine 450  
Bacteria marine isolation antiviral property 1015  
Bacteria methanogenic methyl reductase gene 101  
Bacteria outer membrane vesicle review 607  
Bacteria rhizospheres maize wheat grass cultivars 656  
Bacteria rumen Butyrivibrio taxonomy 274  
Bacteria rumen wall epithelial cell lamb 698  
Bacteria Saccharomyces ribosomal protein gene sequence 164  
Bacteria season change ice Antarctica 329  
Bacterial epiphytic community Laminara digitata 740  
Bacterial growth kinetics radioassay 874  
Bacterial predator soil Arthrobacter prey cell 559  
Bactericide lactoferrin Legionella calcium magnesium 1048  
Bacterioopsin gene regulation Halobacterium review 134  
Bacterioopsin protein gas vesicle mutation Halobacterium 65  
Bacterioplankton phytoplankton coupling eutrophic lake 706  
Bacteriorhodopsin gene mutation Halobacterium 205  
Bacterization plant growth Pseudomonas strain 456  
Bacteroid differentiation Rhizobium pea cellulase 821  
Basidiomycete mycorrhizal saprotrophic revival water 1055  
Basidiospore germination Agaricus bisporus 492  
Bdellovibrios marine salt pond isolation characterization 771  
Bean inoculum density hypocotyl rot 1132  
Bean pea nonlegume rotation Rhizobium leguminosarum 661  
Biochem taxonomy bacteria bone 819  
Bone bacteria biochem taxonomy 819  
Bradyrhizobium japonicum USDA110 USDA122 culture variation 583  
Bradyrhizobium nitrogen fixation nodulation 1156  
Brevibacterium lysine formation dimethyl sulfoxide 668  
Brown pigment Serratia tyrosine metab 1037  
Buccal epithelium glycoprotein Pseudomonas pilus receptor 1141  
Butyrivibrio rumen bacteria taxonomy 274  
Cadmium resistance Neurospora 359  
Calcium alginate Gibberella fujikuroi mycelia immobilization 1118  
Calcium Legionella lactoferrin bactericide 1048  
Calcium Vibrio adhesion intestine cell 642  
Campylobacter cross reacting serotype antigen variation 265  
Candida adhesion cell amphotericin B 260  
Candida infection fibroblast amphotericin B 255  
Carbohydrate Pseudomonas Proteus adhesion hemocyte 524  
Carbon monoxide acetylene redn assay 713  
Carbon nutrition bacteria denitrification soil 754  
Carboxylate Listeria metabolite 786  
Carboxylesterase detn turbidimetry 511  
Catalase gene katB Bacillus mapping 807  
Cation Bacillus diagnosis lepidopteran 444  
Cattle sheep rumen ciliate Canada 686  
Cell Candida adhesion amphotericin B 260  
Cell envelope structure protein Escherichia osmoregulation 843  
Cell HeLa invasion hemolytic G streptococci 515  
Cell intestine Vibrio adhesion calcium acetylglucosamine 642  
Cell NAC1300 infection rabies virus 811  
Cell nucleus eukaryote evolution 109  
Cell prey Arthrobacter bacterial predator soil 559  
Cell survival plasmid Pseudomonas Klebsiella correction 975  
Cell survival plasmid stability Pseudomonas Klebsiella 675  
Cell wall Bacillus metal sorption 764  
Cell wall hydrolase detection bacteria PAGE 749  
Cell yeast flocculent nonflocculent surface characterization 1081  
Cellulase fermn Trichoderma immobilization 968  
Cellulase Rhizobium bacteroid differentiation pea 821  
Cellulolytic microflora rumen lamb 416  
Cellulose degradn Rhizobium pea root nodule 821  
Cephalosporin synthetase ammonium repression Streptomyces 399

- Cephameycin formation *Streptomyces* oxygen iron 1111  
 Chaetomium xylanase I II 836  
 Chlorobenzoate degrading *Pseudomonas* 439  
 Ciliate rumen cattle sheep Canada 686  
 Cladosporium microbody 565  
 Cloning Xylella antigen gene 487  
 Clostridium morphol sorbate hydrochlorate nitrite 388  
 Clostridium perfringens drinking water 932  
 Clostridium protonmotive force selenite transport 481  
 Coliphage human enteric virus drinking water 932  
 Complement killing antigen O K bacteria 994  
 Complementation plasmid *Rhizobium* nonsymbiosis 464  
 Conidia *Neurospora* acid alk phosphatase 830  
 Conjugation plasmid *Streptomyces* 544  
 Corn stunt *Spiroplasma* helicity motility 1087  
 Coronatine gene mutation *Pseudomonas* 910  
 Coronavirus 229E human infectivity pH temp 972  
 Correction amino acid metab *Halobacterium* 748  
 Correction cell survival plasmid *Pseudomonas* *Klebsiella* 975  
 Correction evolution ribosome protein sequence 975  
 Correction hemocyte adhesion *Pseudomonas* *Proteus* carbohydrate 747  
 Correction review bacteria growth limitation 605  
 Cotton decompn *Trichoderma* 469  
 Coupling bacterioplankton phytoplankton eutrophic lake 706  
 Culture media serum free *Spiroplasma* 1092  
 Culture shaken actinomycete morphol 881  
 Culture variation *Bradyrhizobium japonicum* USDA110 USDA122 583  
 Cyclohydrolase methenyltetrahydromethanopterin *Methanobacterium* 499  
 Cysteine proteinase *Trichomonas vaginalis* 903  
 Cytochrome P450 *Saccharomyces* growth 945  
 Cytol *Anabaena* sodium deficiency 322  
 Cytoplasmic membrane antigen *Mycobacterium* 529  
 Cytotoxicity destruxin fungus insect 1000  
 Debaryomyces *hansenii* *Penicillium digitatum* control grapefruit 794  
 Decompn cotton *Trichoderma* 469  
 Dehydrogenase glyceraldehyde phosphate eubacteria eukaryote archaeobacteria 81  
 Dehydrogenase hydroxysteroid kinetics *Escherichia* 1076  
 Dehydrogenase methylenetetrahydromethanopterin *Methanobacterium* 499  
 Dehydrogenase proline *Escherichia* osmotic stress 779  
 Denitrification *Pseudomonas* oxygen 1061  
 Denitrification *Rhizobium* 737  
 Denitrification soil bacteria carbon nutrition 754  
 Deoxymannooctulosonate *Salmonella* lipid A metab 646  
 Desacetoxycycephalosporin C synthase *Streptomyces* oxygen iron 1111  
 Destruxin fungus cytotoxicity insect 1000  
 Desulfurococcus RNA transfer ribosomal intron splicing 210  
 Development ethylene formation respiration *Penicillium* 619  
 Development growth *Physarum* ATP GTP 554  
 Diazinon degrading microorganism yeast 1105  
 Diazotroph establishment maintenance *Sorghum* *Glomus* *Azospirillum* 977  
 Dibenzothiophene biotransformation *Pseudomonas* 603  
 Dicarboxylate metab *Acinetobacter* 1031  
 Dictyostelium mRNA protein spore germination 573  
 Dictyostelium pyrimidine metab 432  
 Dictyostelium spore ribosome rRNA formation 850  
 Differentiation bacteroid *Rhizobium* pea cellulase 821  
 Dimethyl sulfoxide lysine formation *Brevibacterium* 668  
 Dinitrogenase reductase multiple form *Azotobacter* 344  
 Dismutase superoxide gene expression *Halobacterium* 171  
 DNA hybridization *Shewanella* taxonomy 925  
 DNA Lactococcus phage 860  
 DNA methylation *Halobacterium* 205  
 DNA polymerase topoisomerase archaeobacteria review 228  
 DNA protein phage phiPLS743 *Pseudomonas* 630  
 Douglas fir pole fungi colony preservative 283  
 Ecosystem freshwater gene probe microbial population 681  
 Ecosystem soil *Streptomyces* survival effect 535  
 Electrophoresis gram pos bacteria hydrolase detection 749  
 Electrophoresis two dimensional gel protein 960  
 Elongation factor Tu archaeobacteria evolution 2  
 Endonuclease tRNA intron halophilic archaeobacteria 36  
 Enterotoxin *Aeromonas* purin characterization 719  
 Enterotoxin *Escherichia* binding erythrocyte ganglioside 670  
 Enterovirus stability surface freshwater 474  
 Entomophaga aulicae protoplast hemlock looper hemolymph 304  
 Entomophaga protoplast protein formation 373  
 Environment genetic engineering microorganism review 895  
 Epiphytic bacterial community *Laminaria digitata* 740  
 Epithelial cell rumen wall bacteria lamb 698  
 Epithelium buccal glycoprotein *Pseudomonas* pilus receptor 1141  
 Erwinia pectate lyase monoclonal antibody 651  
 Erythrocyte *Escherichia* enterotoxin binding ganglioside 670  
*Escherichia* cell envelope structure protein osmoregulation 843  
*Escherichia coli* nutrient response seawater 379  
*Escherichia* enterotoxin binding erythrocyte ganglioside 670  
*Escherichia* gene *murE* sequence 1051  
*Escherichia* hydroxysteroid dehydrogenase kinetics 1076  
*Escherichia* lipopolysaccharide O deficient mutant 994  
*Escherichia* osmotic stress proline dehydrogenase 779  
*Escherichia* outer membrane permeability far UV 1022  
*Escherichia* sensitivity antibiotic AS48 318  
*Escherichia* Shiga toxin variant *ferm*n 623  
 Esterase detn turbidimetry Tween 20 511  
 Ether alkyl metab *Acinetobacter* 1031  
 Ethylene cycling nitrogenase detn forest soil 713  
 Ethylene formation development respiration *Penicillium* 619  
 Ethylene formation *Penicillium* 384  
 Eubacteria glyceraldehyde phosphate dehydrogenase eukaryote archaeobacteria 81  
 Eubacteria *Methanococcus* ribosome protein gene sequence 11  
 Eubacteria RNA polymerase evolution archaeobacteria eukaryote 73  
 Eubacteria surface protein organization review 215  
 Eukaryote cell nucleus evolution 109  
 Eukaryote glyceraldehyde phosphate dehydrogenase eubacteria archaeobacteria 81  
 Eukaryote RNA polymerase evolution archaeobacteria eubacteria 73  
 Evolution archaeobacteria 119  
 Evolution archaeobacteria ribosome 141  
 Evolution DNA topoisomerase archaeobacteria review 228  
 Evolution elongation factor Tu archaeobacteria 2  
 Evolution eukaryote cell nucleus 109  
 Evolution glyceraldehyde phosphate dehydrogenase homol urkingdom 81  
 Evolution ribosome protein sequence 234  
 Evolution ribosome protein sequence correction 975  
 Evolution RNA polymerase archaeobacteria eubacteria eukaryote 73  
 Evolution 5S rRNA structure archaeobacteria 43  
 Far UV outer membrane permeability *Escherichia* 1022  
 Fatty acid *Leptospira* skin reaction 1009  
 Fenitrothion degrading microorganism yeast 1105  
 Fibroblast *Candida* infection amphotericin B 255  
 Filtration drinking water microorganism virus 932  
 Filtration water reverse osmosis bacteria colonization 1065  
 Flagella antibody opsonophagocytosis *Pseudomonas* 890  
 Flavin redn *Azotobacter* metronidazole 340  
 Flocculent nonflocculent yeast cell surface characterization 1081  
 Forest soil nitrogenase detn ethylene cycling 713  
*Francisella tularensis* growth survival *Acanthamoeba palestinensis* 1100  
*Frankia* respiration hydrogenase nitrogenase 636  
*Frankia* spore germination life cycle 801  
 Freshwater surface enterovirus stability 474  
 Fungi colony Douglas fir pole preservative 283  
 Fungi galacturonic acid distribution *Aplysia* depilans 349  
 Fungus destruxin cytotoxicity insect 1000  
 Galacturonic acid distribution fungi *Aplysia* depilans 349  
*Galleria* cytotoxicity destruxin fungus 1000  
 Ganglioside *Escherichia* enterotoxin binding erythrocyte 670  
 Gas vesicle purple membrane mutation *Halobacterium* 65  
 Gel two dimensional electrophoresis protein 960  
 Gene antigen Xylella cloning 487  
 Gene bacterioopsin regulation *Halobacterium* review 134  
 Gene bacteriorhodopsin mutation *Halobacterium* 205  
 Gene coronatine mutation *Pseudomonas* 910  
 Gene *gyp* bop *Halobacterium* mutation 65  
 Gene *Halobacterium* mapping 21  
 Gene *Halobacterium* phage phiH review 182  
 Gene *katB* catalase *Bacillus* mapping 807  
 Gene mapping *Aspergillus* *Novozym* enrichment 982  
 Gene *mcr* conservation methanogenic archaeobacteria 52  
 Gene methionine tRNA intron *Halobacterium* 189  
 Gene methyl reductase methanogenic bacteria 101  
 Gene *murE* sequence *Escherichia* 1051  
 Gene probe microbial population freshwater ecosystem 681  
 Gene ribosomal protein *Methanococcus* review 200  
 Gene ribosomal protein sequence bacteria *Saccharomyces* 164  
 Gene ribosome protein sequence *Halobacterium* 153  
 Gene ribosome protein sequence *Methanococcus* eubacteria 11  
 Gene RNA polymerase archaeobacteria eubacteria eukaryote 73  
 Gene rRNA polymorphism *Achlya* 1146  
 Gene sequence pHSB1 plasmid *Halobacterium* 86  
 Gene superoxide dismutase expression *Halobacterium* 171  
 Gene transfer pilus plasmid pH1508a mapping 289  
 Gene vac mutation plasmid *Halobacterium* 96

- Gene 16S rRNA sequence *Thermoplasma* 124  
 Genetic engineering microorganism environment review 895  
 Germination basidiospore *Agaricus bisporus* 492  
 Germination spore *Dictyostelium* mRNA protein 573  
 Germination spore life cycle *Frankia* 801  
 Germination spore *Neurospora* phosphatase control 830  
 Germination spore ribosome formation *Dictyostelium* 850  
*Giardia lamblia* cyst drinking water 932  
*Gibberella fujikuroi* mycelia immobilization calcium alginate 1118  
*Glomus Azospirillum Sorghum* diazotroph establishment maintenance 977  
 Glucose triggering spore *Bacillus* alanine inosine 760  
 Glycanase phage lipopolysaccharide O deficient mutant 994  
 Glyceraldehyde phosphate dehydrogenase eubacteria eukaryote archaeobacteria 81  
 Glycoprotein buccal epithelium *Pseudomonas pilus* receptor 1141  
 Glycoprotein deficiency interferon vesicular stomatitis virus 334  
 Gram pos bacteria hydrolase detection electrophoresis 749  
 Grapefruit *Debaryomyces hansenii* *Penicillium digitatum* control 794  
 Grass maize wheat cultivars bacteria rhizospheres 656  
 Groundwater pollution petroleum heterotrophic activity 814  
 Growth development *Physarum* ATP GTP 554  
 Growth sugar metab *Listeria* 245  
 Growth survival *Francisella tularensis* *Acanthamoeba palestinensis* 1100  
 GTP ATP *Physarum* growth development 554  
 Halobacterium amino acid metab 508  
 Halobacterium bacteriopsin gene regulation review 134  
 Halobacterium gene mapping 21  
 Halobacterium methionine tRNA gene intron 189  
 Halobacterium mutation bacteriorhodopsin gene 205  
 Halobacterium phage phiH gene review 182  
 Halobacterium plasmid 92  
 Halobacterium plasmid gene vac mutation 96  
 Halobacterium plasmid pHSB polymorphism 160  
 Halobacterium plasmid pHSB1 gene sequence 86  
 Halobacterium purple membrane gas vesicle mutation 65  
 Halobacterium ribosome protein gene sequence 153  
 Halobacterium ribosome protein sequence 195 234  
 Halobacterium spheroplast transformation 148  
 Halobacterium superoxide dismutase gene expression 171  
 Halocin formation *Halobacterium* 205  
 Halophilic archaeobacteria tRNA intron processing endonuclease 36  
 HeLa cell invasion hemolytic *G streptococci* 515  
 Helicity motility corn stunt *Spiroplasma* 1087  
 Hemlock looper hemolymph *Entomophaga aulicae* protoplast 304  
 Hemocyte adhesion *Pseudomonas Proteus* carbohydrate 524  
 Hemocyte adhesion *Pseudomonas Proteus* carbohydrate correction 747  
 Hemolymph hemlock looper *Entomophaga aulicae* protoplast 304  
 Hemolytic *G streptococci* HeLa cell invasion 515  
 Heterotrophic activity groundwater pollution petroleum 814  
 Human coronavirus 229E infectivity pH temp 972  
 Human enteric virus coliphage drinking water 932  
 Hybridization DNA *Shewanella* taxonomy 925  
 Hydrochlorate *Clostridium* morphol 388  
 Hydrogenase nitrogenase respiration *Frankia* 636  
 Hydrolase detection cell wall bacteria PAGE 749  
 Hydroponic culture rhizosphere microbial development 456  
 Hydroxysteroid dehydrogenase kinetics *Escherichia* 1076  
 Hypocotyl rot inoculum density *Rhizoctonia solani* 1132  
 Ice bacteria season change Antarctica 329  
 Immobilization *Trichoderma cellulase* fermn 968  
 Immunol differentiation *Penicillium* 1043  
 Infection NAC1300 cell rabies virus 811  
 Infectivity human coronavirus 229E pH temp 972  
 Inoculum density hypocotyl rot *Rhizoctonia solani* 1132  
 Inosine alanine *Bacillus* glucose triggering spore 760  
 Insect cytotoxicity fungus destruxin 1000  
 Insecticide phosphorus degradn microorganism yeast 1105  
 Insertion sequence gene mutation *Halobacterium* 65  
 Interferon vesicular stomatitis virus glycoprotein deficiency 334  
 Intestinal anaerobic bacteria methanol inhibition 313  
 Intestine cell *Vibrio* adhesion calcium acetylglucosamine 642  
 Intestine microflora newborn rat *Staphylococci* 989  
 Intron methionine tRNA gene *Halobacterium* 189  
 Intron splicing RNA transfer ribosomal *Desulfurococcus* 210  
 Intron tRNA processing endonuclease halophilic archaeobacteria 36  
 Iodine sensitivity bacteria 520  
 Iron binding agent *Saccharomyces* 845  
 Iron *Streptomyces* cephamycin formation 1111  
 Isocitrate dehydrogenase *Bacillus surfactin* fermn 854  
 Isopenicillin N synthase *Streptomyces* oxygen iron 1111  
 K antigen bacteria complement killing 994  
 Kinetics bacterial growth radioassay 874  
 Klebsiella lipopolysaccharide O deficient mutant 994  
 Klebsiella *Pseudomonas* cell survival plasmid stability 675  
 Klebsiella transformation lipopolysaccharide O antigen 735  
 Lactate bacteria spermine 450  
 Lactococcus phage DNA protein 860  
 Lactoferrin bactericide *Legionella* calcium magnesium 1048  
 Lactoferrin binding protein *Neisseriaceae* 409  
 Lake eutrophic coupling bacterioplankton phytoplankton 706  
 Lamb bacteria rumen wall epithelial cell 698  
 Lamb rumen cellulolytic microflora 416  
 Laminara digitata epiphytic bacterial community 740  
 Legionella lactoferrin bactericide calcium magnesium 1048  
 Legionella pneumophila drinking water 932  
 Lepidopteran *Bacillus* diagnosis cation 444  
 Leptospira lipid skin reaction 1009  
 Life cycle spore germination *Frankia* 801  
 Lipase detn turbidimetry Tween 20 511  
 Lipid A metab *Salmonella* deoxymannooctulosonate 646  
 Lirid Leptospira skin reaction 1009  
 Lipopolysaccharide O antigen Klebsiella transformation 735  
 Lipopolysaccharide O deficient mutant glycanase phage 994  
 Listeria growth sugar metab 245  
 Listeria metabolite carboxylate amine 786  
 Lyase pectate monoclonal antibody *Erwinia* 651  
 Lysine formation dimethyl sulfoxide *Brevibacterium* 668  
 Macroptilium *Vigna* nodulation *Bradyrhizobium* 1156  
 Magnesium *Legionella* lactoferrin bactericide 1048  
 Maize wheat grass cultivars bacteria rhizospheres 656  
 Mapping gene *Aspergillus* *Novozym* enrichment 982  
 Mapping gene katB catalase *Bacillus* 807  
 Mapping *Halobacterium* gene 21  
 Mapping plasmid pHH1508a transfer pilus gene 289  
 Marine bacteria isolation antiviral property 1015  
 Marine salt pond isolation characterization *bdellovibrios* 771  
 Melanin formation *Phaeoocomyces* 728  
 Membrane outer vesicle bacteria review 607  
 Membrane purple gas vesicle mutation *Halobacterium* 65  
 Metal sorption cell wall *Bacillus* 764  
 Metarhizium destruxin cytotoxicity insect 1000  
 Methanobacterium methyl reductase gene 101  
 Methanobacterium methylenetetrahydromethanopterin dehydrogenase 499  
 Methanobacterium pseudomurein formation 176  
 Methanobacterium RNA polymerase gene 52  
 Methanococcus eubacteria ribosome protein gene sequence 11  
 Methanococcus methyl reductase gene 101  
 Methanococcus promoter sequence detn 30  
 Methanococcus ribosomal protein gene review 200  
 Methanogenic archaeobacteria gene mcr conservation 52  
 Methanogenic bacteria methyl reductase gene 101  
 Methanogenesis inhibition anaerobic intestinal bacteria 313  
 Methanosarcina methyl reductase gene 101  
 Methanothermobacter methyl reductase gene 101  
 Methylenetetrahydromethanopterin cyclohydrolase *Methanobacterium* 499  
 Methionine tRNA gene intron *Halobacterium* 189  
 Methyl coenzyme M reductase gene conservation 52  
 Methyl parathion degradn microorganism yeast 1105  
 Methyl reductase gene methanogenic bacteria 101  
 Methylation DNA *Halobacterium* 205  
 Methylenetetrahydromethanopterin dehydrogenase *Methanobacterium* 499  
 Metronidazole *Azotobacter* flavin redn 340  
 Microbial development rhizosphere hydroponic culture 456  
 Microbial population gene probe freshwater ecosystem 681  
 Microbody *Cladosporium* 565  
 Microflora cellulolytic rumen lamb 416  
 Microflora intestine newborn rat *Staphylococci* 989  
 Microorganism genetic engineering environment review 895  
 Microorganism oxoaldehyde metab review 423  
 Microorganism phosphorus insecticide degradn yeast 1105  
 Microorganism population mineral hardness Ontario river 744  
 Microorganism virus filtration drinking water 932  
 Mineral hardness population microorganism Ontario river 744  
 Monoclonal antibody pectate lyase *Erwinia* 651  
 Monoclonal antibody poliovirus 550  
 Morphol actinomycete shaken culture 881  
 Motility helicity corn stunt *Spiroplasma* 1087  
 mRNA protein spore germination *Dictyostelium* 573  
 Mutacin formation *Streptococcus* 366  
 Mutation bacteriorhodopsin gene *Halobacterium* 205  
 Mutation coronatine gene *Pseudomonas* 910  
 Mutation gene vac plasmid *Halobacterium* 96  
 Mutation purple membrane gas vesicle *Halobacterium* 65  
 Mycelia *Gibberella fujikuroi* immobilization calcium alginate 1118  
 Mycobacterium antigen cytoplasmic membrane 529



- Mycorrhizal basidiomycete saprotrophic revival water 1055  
 NAC1300 cell infection rabies virus 811  
 Neisseria arginine proline auxotroph 1069  
 Neisseriaceae transferrin lactoferrin binding protein 409  
 Nematode soil trophozoites *Theratomyxa weberi* predacious 589  
 Neurospora cadmium resistance 359  
 Neurospora conidia acid alk phosphatase 830  
 Nitrate reductase *Pseudomonas* oxygen 1061  
 Nitrite *Clostridium* morphol 388  
 Nitrite reductase *Pseudomonas* oxygen 1061  
 Nitrogen fixation nodulation *Bradyrhizobium* 1156  
 Nitrogen fixation rice *Alcaligenes* 403  
 Nitrogenase detn forest soil ethylene cycling 713  
 Nitrogenase hydrogenase respiration *Frankia* 636  
 Nodulation nitrogen fixation *Bradyrhizobium* 1156  
 Nonfloculent flocculent yeast cell surface characterization 1081  
 Nonlegume bean pea rotation *Rhizobium* leguminosarum 661  
 Nonsclerotial pathogenic mutant *Sclerotinia sclerotiorum* 517  
 Novozym enrichment gene mapping *Aspergillus* 982  
 Nucleus cell eukaryote evolution 109  
 Nutrient response *Escherichia coli* seawater 379  
 O antigen bacteria complement killing 994  
 Opsonophagocytosis flagella antibody *Pseudomonas* 890  
 Osmosis reverse water filtration bacteria colonization 1065  
 Osmotic stress *Escherichia* proline dehydrogenase 779  
 Outer membrane *Escherichia* permeability far UV 1022  
 Oxaldehyde metab microorganism review 423  
 Oxygen *Pseudomonas* denitrification 1061  
 Oxygen *Streptomyces* cephamycin formation 1111  
 Paraquat superoxide dismutase gene *Halobacterium* 171  
 Parathion degrdn microorganism yeast 1105  
 Pea bean nonlegume rotation *Rhizobium* leguminosarum 661  
 Pea root nodule cellulose degrdn *Rhizobium* 821  
 Pectate lyase monoclonal antibody *Erwinia* 651  
 Penicillium digitatum control grapefruit *Debaryomyces hansenii* 794  
 Penicillium ethylene formation 384  
 Penicillium immunol differentiation 1043  
 Penicillium respiration ethylene formation development 619  
 Peptostreptococcus albumin binding 614  
 Permeability outer membrane *Escherichia* far UV 1022  
 Petroleum product groundwater pollution heterotrophic 814  
 Phaeococcomycetes melanin formation 728  
 Phage glycanase lipopolysaccharide O deficient mutant 994  
 Phage *Lactococcus* DNA protein 860  
 Phage phiH gene *Halobacterium* review 182  
 Phage phiPLS743 DNA protein *Pseudomonas* 630  
 pHH1508a plasmid transfer pilus gene mapping 289  
 PhiPLS743 phage DNA protein *Pseudomonas* 630  
 Phosphatase acid alk conidia *Neurospora* 830  
 Phosphoribosyltransferase adenine *Physarum* 554  
 Phosphorus insecticide degrdn microorganism yeast 1105  
 Phosphorylase adenosine *Physarum* 554  
 pHSB1 plasmid gene sequence *Halobacterium* 86  
*Physarum* growth development ATP GTP 554  
 Phytoplankton bacterioplankton coupling eutrophic lake 706  
 Phytotoxin coronatine formation *Pseudomonas* 910  
 Pigment brown *Serratia* tyrosine metab 1037  
 Pilus gene mapping plasmid pHH1508a 289  
 Pilus *Pseudomonas* receptor buccal epithelium glycoprotein 1141  
 Plant growth bacterization *Pseudomonas* strain 456  
 Plasmid complementation *Rhizobium* nonsymbiosis 464  
 Plasmid conjugation *Streptomyces* 544  
 Plasmid gene vac mutation *Halobacterium* 96  
 Plasmid *Halobacterium* 92  
 Plasmid pHH1508a transfer pilus gene mapping 289  
 Plasmid pHSB polymorphism *Halobacterium* 160  
 Plasmid pHSB1 gene sequence *Halobacterium* 86  
 Plasmid stability cell survival *Pseudomonas* *Klebsiella* 675  
 Plasmid stability *Pseudomonas* soil 951  
 Poliovirus monoclonal antibody 550  
 Pollution groundwater petroleum heterotrophic activity 814  
 Polymerase DNA archaeobacteria review 228  
 Polymerase RNA evolution archaeobacteria eubacteria eukaryote 73  
 Polymerase RNA gene *Methanobacterium* 52  
 Polymorphism rRNA gene *Achlya* 1146  
 Polysaccharide *Pseudomonas* adhesion detachment 309  
 Pond salt marine isolation characterization *bdellovibrios* 771  
 Predation protozoan bacteria abundance 578  
 Predator bacterial soil *Arthrobacter* prey cell 559  
 Preservative Douglas fir pole fungi 283  
 Prey cell *Arthrobacter* bacterial predator soil 559  
 Probe gene microbial population freshwater ecosystem 681  
 Processing tRNA intron endonuclease halophilic archaeobacteria 36  
 Proline arginine auxotroph *Neisseria* 1069  
 Proline dehydrogenase *Escherichia* osmotic stress 779  
 Promoter sequence detn archaeobacteria 30  
 Prophenoeloxidase *Pseudomonas* *Proteus* adhesion hemocyte 524  
 Protein cell envelope *Escherichia* osmoregulation 843  
 Protein DNA phage phiPLS743 *Pseudomonas* 630  
 Protein elongation factor gene *Methanococcus* review 200  
 Protein formation *Entomophaga* protoplast 373  
 Protein *Lactococcus* phage 860  
 Protein mRNA spore germination *Dictyostelium* 573  
 Protein ribosomal gene sequence bacteria *Saccharomyces* 164  
 Protein ribosome gene sequence *Halobacterium* 153  
 Protein ribosome gene sequence *Methanococcus* eubacteria 11  
 Protein sequence ribosome evolution 234  
 Protein sequence ribosome *Halobacterium* 195  
 Protein surface organization eubacteria archaeobacteria review 215  
 Protein transferrin lactoferrin binding *Neisseriaceae* 409  
 Protein two dimensional gel electrophoresis 960  
 Proteinase A B Y yeast 295  
 Proteinase cysteine *Trichomonas vaginalis* 903  
*Proteus* *Pseudomonas* carbohydrate adhesion hemocyte 524  
 Proton efflux wheat root *Azospirillum* 691  
 Protonmotive force selenite transport *Clostridium* 481  
 Protoplast *Entomophaga* aulicae hemlock looper hemolymph 304  
 Protoplast *Entomophaga* protein formation 373  
 Protozoan predation bacteria abundance 578  
*Pseudomonas* chlorobenzoate degrdn 439  
*Pseudomonas* coronatine gene mutation 910  
*Pseudomonas* denitrification oxygen 1061  
*Pseudomonas* dibenzothioephene biotransformation 603  
*Pseudomonas* flagella antibody opsonophagocytosis 890  
*Pseudomonas* iodine sensitivity 520  
*Pseudomonas* *Klebsiella* cell survival plasmid stability 675  
*Pseudomonas* phage phiPLS743 DNA protein 630  
*Pseudomonas* pilus receptor buccal epithelium glycoprotein 1141  
*Pseudomonas* plasmid stability soil 951  
*Pseudomonas* polysaccharide adhesion detachment 309  
*Pseudomonas* *Proteus* carbohydrate adhesion hemocyte 524  
*Pseudomonas* soil core microcosm Tn5 mutant 867  
*Pseudomonas* strain plant growth bacterization 456  
 Pseudomurein formation *Methanobacterium* 176  
 Purple membrane gas vesicle mutation *Halobacterium* 65  
 Pyrimidine metab *Dictyostelium* 432  
 Rabies virus infection NAC1300 cell 811  
 Radioassay bacterial growth kinetics 874  
 Rat newborn intestine microflora *Staphylococci* 989  
 Receptor *Pseudomonas* pilus buccal epithelium glycoprotein 1141  
 Reductase dinitrogenase multiple form *Azotobacter* 344  
 Reductase methyl coenzyme M gene conservation 52  
 Reductase methyl gene methanogenic bacteria 101  
 Reductase nitrate nitrite *Pseudomonas* oxygen 1061  
 Respiration *Azotobacter* aeration 918  
 Respiration ethylene formation development *Penicillium* 619  
 Respiration hydrogenase nitrogenase *Frankia* 636  
 Reverse osmosis water filtration bacteria colonization 1065  
 Review archaeobacteria DNA polymerase topoisomerase 228  
 Review bacteria growth limitation correction 605  
 Review bacteria outer membrane vesicle 607  
 Review bacteriopsis gene regulation *Halobacterium* 134  
 Review environment microbial genetics 895  
 Review *Halobacterium* phage phiH gene 182  
 Review metab archaeobacteria 58  
 Review oxaldehyde metab microorganism 423  
 Review ribosomal protein gene *Methanococcus* 200  
 Review surface protein organization eubacteria archaeobacteria 215  
*Rhizobium* cellulose degrdn pea root nodule 821  
*Rhizobium* denitrification 737  
*Rhizobium* leguminosarum bean pea nonlegume rotation 661  
*Rhizobium* nonsymbiosis complementation plasmid 464  
*Rhizoctonia solani* inoculum density hypocotyl rot 1132  
 Rhizosphere microbial development hydroponic culture 456  
 Rhizospheres maize wheat grass cultivars bacteria 656  
 Ribosomal protein gene *Methanococcus* review 200  
 Ribosomal protein gene sequence bacteria *Saccharomyces* 164  
 Ribosome archaeobacteria evolution 141  
 Ribosome protein gene sequence *Halobacterium* 153  
 Ribosome protein gene sequence *Methanococcus* eubacteria 11  
 Ribosome protein sequence evolution 234  
 Ribosome protein sequence *Halobacterium* 195  
 Ribosome rRNA formation *Dictyostelium* spore 850  
 Rice nitrogen fixation *Alcaligenes* 403  
 River Ontario mineral hardness population microorganism 744  
 RNA polymerase evolution archaeobacteria eubacteria eukaryote 73  
 RNA polymerase gene *Methanobacterium* 52  
 RNA transfer ribosomal intron splicing *Desulfurococcus* 210  
 Root growth inhibitor *Pseudomonas* Tn5 mutant 867  
 Root hair *Azospirillum* adsorption 936  
 Root nodule pea cellulose degrdn *Rhizobium* 821



- Root proton efflux wheat *Azospirillum* 691  
 rRNA formation ribosome *Dictyostelium* spore 850  
 rRNA gene polymorphism *Achlya* 1146  
 rRNA intron splicing *Desulfurococcus* 210  
 rRNA 16S gene sequence *Thermoplasma* 124  
 rRNA 5S structure evolution archaeobacteria 43  
 Rumen ciliate cattle sheep Canada 686  
 Rumen lamb cellulolytic microflora 416  
 Rumen wall epithelial cell lamb bacteria 698  
*Saccharomyces* bacteria ribosomal protein gene sequence 164  
*Saccharomyces* growth cytochrome P450 945  
*Saccharomyces* proteinase A B Y 295  
*Salmonella* lipid A metab deoxymannoculosonate 646  
 Saprotrophic mycorrhizal basidiomycete revival water 1055  
 Season change bacteria ice Antarctica 329  
 Seawater *Escherichia coli* nutrient response 379  
 Secondary structure Ur 5S rRNA 43  
 Selenite transport protonmotive force *Clostridium* 481  
 Sequence gene murE *Escherichia* 1051  
 Sequence homol glyceraldehyde phosphate dehydrogenase urkingdom 81  
 Sequence methionine tRNA gene *Halobacterium* 189  
 Sequence plasmid pHSB1 gene *Halobacterium* 86  
 Sequence promoter detn archaeobacteria 30  
 Sequence protein ribosome evolution 234  
 Sequence ribosomal protein gene bacteria *Saccharomyces* 164  
 Sequence ribosome protein gene *Halobacterium* 153  
 Sequence ribosome protein gene *Methanococcus* eubacteria 11  
 Sequence ribosome protein *Halobacterium* 195  
 Sequence RNA polymerase archaeobacteria eubacteria eukaryote 73  
 Sequence rRNA 16S gene *Thermoplasma* 124  
 Serotype cross reacting *Campylobacter* antigen variation 265  
*Serratia* brown pigment tyrosine metab 1037  
 Serum free culture media spiroplasma 1092  
 Sheep cattle rumen ciliate Canada 686  
*Shewanella* taxonomy DNA hybridization 925  
 Shiga toxin variant fermn *Escherichia* 623  
 Skin reaction *Leptospira* lipid 1009  
 Sodium deficiency *Anabaena* cytol 322  
 Soil *Arthrobacter* prey cell bacterial predator 559  
 Soil core microcosm Tn5 mutant *Pseudomonas* 867  
 Soil denitrification bacteria carbon nutrition 754  
 Soil ecosystem *Streptomyces* survival effect 535  
 Soil nematode trophozoites *Theratomyxa weberi* predacious 589  
 Soil *Pseudomonas* plasmid stability 951  
 Sorbate *Clostridium* morphol 388  
 Sorghum *Glomus Azospirillum* diazotroph establishment maintenance 977  
 Sorption metal cell wall *Bacillus* 764  
 Spermine *Bacillus* 450  
 Spheroplast *Halobacterium* transformation 148  
*Spiroplasma kunkelii* helicity motility 1087  
*Spiroplasma* serum free culture media 1092  
 Splicing intron RNA transfer ribosomal *Desulfurococcus* 210  
 Spore germination *Dictyostelium* mRNA protein 573  
 Spore germination life cycle *Frankia* 801  
 Spore germination *Neurospora* phosphatase control 830  
 Spore germination ribosome formation *Dictyostelium* 850  
 Spore glucose triggering *Bacillus* alanine inosine 760  
*Staphylococci* intestine microflora newborn rat 989  
*Streptococci* hemolytic G HeLa cell invasion 515  
*Streptococcus* mutacin formation 366  
*Streptomyces* ammonium repression cephalosporin synthetase 399  
*Streptomyces* cephamycin formation oxygen iron 1111  
*Streptomyces* plasmid conjugation 544  
*Streptomyces* survival effect soil ecosystem 535  
 Sugar metab growth *Listeria* 245  
*Sulfolobus* ribosome protein sequence 234  
 Superoxide dismutase gene expression *Halobacterium* 171  
 Surface characterization flocculent nonflocculent yeast cell 1081  
 Surface protein organization eubacteria archaeobacteria review 215  
 Surfactin fermn *Bacillus* isocitrate dehydrogenase 854  
 Survival growth *Francisella tularensis* *Acanthamoeba palestinensis* 1100  
 Synthetase cephalosporin ammonium repression *Streptomyces* 399  
 Taxonomy biochem bacteria bone 819  
 Taxonomy *Butyrivibrio* rumen bacteria 274  
 Taxonomy *Shewanella* DNA hybridization 925  
*Theratomyxa weberi* predacious trophozoites soil nematode 589  
*Thermoplasma* rRNA 16S gene sequence 124  
 Tn5 mutant *Pseudomonas* soil core microcosm 867  
 Topoisomerase DNA evolution property archaeobacteria review 228  
 Toxin Shiga variant fermn *Escherichia* 623  
 Transcription factor archaeobacteria 30  
 Transfer gene mapping plasmid pHH1508a 289  
 Transferrin binding protein *Neisseriaceae* 409  
 Transformation *Halobacterium* 205  
 Transformation *Klebsiella lipopolysaccharide* O antigen 735  
 Transformation spheroplast *Halobacterium* 148  
 Transport selenite protonmotive force *Clostridium* 481  
*Trichoderma* decompn cotton 469  
*Trichoderma* immobilization cellulase fermn 968  
*Trichomonas* cysteine proteinase vaginalis 903  
 tRNA intron processing endonuclease halophilic archaeobacteria 36  
 tRNA intron splicing *Desulfurococcus* 210  
 tRNA methionine gene intron *Halobacterium* 189  
 Trophozoites *Theratomyxa weberi* predacious soil nematode 589  
 Turbidimetry esterase lipase detn Tween 20 511  
 Tween 20 esterase lipase detn turbidimetry 511  
 Two dimensional gel electrophoresis protein 960  
 Tyrosine metab *Serratia* brown pigment 1037  
 Ur 5S rRNA secondary structure 43  
 USDA110 USDA122 *Bradyrhizobium japonicum* culture variation 583  
 USDA122 USDA110 *Bradyrhizobium japonicum* culture variation 583  
 UV far outer membrane permeability *Escherichia* 1022  
 Vaginalis *Trichomonas* cysteine proteinase 903  
 Vesicle gas purple membrane mutation *Halobacterium* 65  
 Vesicle outer membrane bacteria review 607  
 Vesicular stomatitis virus glycoprotein deficiency interferon 334  
*Vibrio* adhesion intestine cell calcium acetylglucosamine 642  
*Vigna Macroptilium* nodulation *Bradyrhizobium* 1156  
 Virus microorganism filtration drinking water 932  
 Virus rabies infection NAC1300 cell 811  
 Virus vesicular stomatitis glycoprotein deficiency interferon 334  
 Wall cell *Bacillus* metal sorption 764  
 Water drinking microorganism virus filtration 932  
 Water filtration reverse osmosis bacteria colonization 1065  
 Water saprotrophic mycorrhizal basidiomycete revival 1055  
 Wheat grass maize cultivars bacteria rhizospheres 656  
 Wheat root proton efflux *Azospirillum* 691  
 Xylanase I II *Chaetomium* 836  
 Xylella antigen gene cloning 487  
 Yeast cell flocculent nonflocculent surface characterization 1081  
 Yeast phosphorus insecticide degrading microorganism 1105  
 Yeast proteinase A B Y 295